

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 24, 1999, 01:30:01 ; Search time 366.45 seconds  
(without alignments)  
1435.120 Million cell updates/sec

Title: US-09-205-015-2

Perfect score: 147

Sequence: 1 agataactgggccaaccatg.....ctcccccctctgtttatct 147

Scoring table: IDENTITY\_NUC

Searched: 808301 seqs, 178873984 residues

Database :

GenEmbl.\*

1: gb\_ba1.\*

2: gb\_ba2.\*

3: gb\_in.\*

4: gb\_ov.\*

5: gb\_ov.\*

6: gb\_ov.\*

7: gb\_ph.\*

8: gb\_ph.\*

9: gb\_pl1.\*

10: gb\_pl2.\*

11: gb\_pr2.\*

12: gb\_pr3.\*

13: gb\_ro.\*

14: gb\_st.\*

15: gb\_sy.\*

16: gb\_un.\*

17: gb\_vl.\*

18: gb\_hlg.\*

19: gb\_ba.\*

20: gb\_fun.\*

21: gb\_hum1.\*

22: gb\_hum2.\*

23: gb\_in.\*

24: gb\_ov.\*

25: gb\_ov.\*

26: gb\_ov.\*

27: gb\_pat.\*

28: gb\_ph.\*

29: gb\_pl.\*

30: gb\_ro.\*

31: gb\_sy.\*

32: gb\_un.\*

33: gb\_vl.\*

34: gb\_hlg.\*

35: gb\_ba.\*

36: gb\_ba.\*

37: gb\_ba.\*

38: gb\_pl1.\*

39: gb\_pl2.\*

40: gb\_pr1.\*

41: gb\_pr2.\*

42: gb\_pr3.\*

43: gb\_st.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
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ALIGNMENTS

RESULT 1

S49899

LOCUS

DEFINITION

ACCSSION

NID

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REMARK

COMMENT

S49899 356 bp DNA PRI 10-JUL-1992  
alpha-globin gene cluster: [5' region, major regulatory element]  
[human, Genomic, 356 nt].

S49899

g233777

human.

Homo sapiens

Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;

Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 356)

Jarman,A.P., Wood,W.G., Sharpe,J.A., Gourdon,G., Ayub,H. and

Higgs,D.R.

Characterization of the major regulatory element upstream of the

human alpha-globin gene cluster

Mol. Cell. Biol. 11 (9), 4679-4689 (1991)

91342671

GenBank staff at the National Library of Medicine created this

entry [NCBI gbbsq 49899] from the original journal article.

This sequence comes from fig 5.

Region: alpha-globin gene cluster.

1 145.4 98.9 356 10 S49899  
2 145.4 98.9 19226 11 HSG64  
3 145.4 98.9 356 40 S49899  
4 145.4 98.9 19226 41 HSG64  
5 70.2 47.8 277 13 S78508  
6 70.2 47.8 330 13 MMT08220  
7 31 21.1 9750 12 HSU1  
8 31 21.1 9750 42 HSU1  
9 30.6 20.8 1149 10 HSPKCG5  
10 30.6 20.8 1149 40 HSPKCG5  
11 30.4 20.7 40668 11 AC003112  
12 30.4 20.7 118313 11 AC003991  
13 30.4 20.7 239269 18 AC004953  
14 30.4 20.7 198776 18 AC005075  
15 30.4 20.7 40668 41 AC003112  
16 30.4 20.7 118313 41 AC003991  
17 30.2 20.5 5289 11 AB014533  
18 30.2 20.5 115045 11 AC004414  
19 30.2 20.5 5289 41 AB014533  
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22 30 20.4 97904 18 AC005705  
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29 29.2 19.9 89818 11 AC002126  
30 29.2 19.9 50511 11 AC005214  
31 29.2 19.9 34877 11 CH19R37740  
32 29.2 19.9 71353 12 AF104455  
33 29.2 19.9 1961 13 AB013455  
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36 29.2 19.9 170891 18 AC002118  
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38 29.2 19.9 89818 41 AC002126  
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41 29.2 19.9 71353 42 AF104455  
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45 29 19.7 1315 13 MUSTCPWC

S49899 alpha-globi  
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S49899 alpha-globi  
284722 Human DNA s  
S78508 alpha globi  
U08220 Mus musculu  
U73778 Human colla  
X62533 H.sapiens g  
X62533 H.sapiens g  
AC003112 Human DNA  
AC003991 Human DNA  
AC004953 \*\*\* SEQUE  
AC005075 \*\*\* SEQUE  
AC003112 Human DNA  
AC003991 Human DNA  
AB014533 Homo sapi  
AC004414 Homo sapi  
AB014533 Homo sapi  
AC004414 Homo sapi  
AC005440 \*\*\* SEQUE  
AC005705 \*\*\* SEQUE  
L14565 Human perip  
AC004990 Homo sapi  
L14565 Human perip  
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254140 S.pombe chr  
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AC005214 Homo sapi  
AD000812 Homo sapi  
AF104455 Homo sapi  
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L13257 Rattus norv  
M90514 Rattus ratt  
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AC005214 Homo sapi  
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Best Local Similarity 99.3%; Pred. No. 7.4e-38;
Matches 146; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 agataactgggccaacatgactcagctctctggaggccaacagagctctgagtcac 60
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QY 61 ctgtgggggtggagtgagggaaggaagggtggaatgctgctgattacaacctct 120
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QY 121 ggtgctgcctccctcctcttattct 147
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Db 231 GGTGCTGCCTCCCTCCTCTGTTATCT 257
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RESULT 2
HSGG4      19226 bp      DNA      PRI      19-MAR-1997
LOCUS      Human DNA sequence from cosmid GG4 from a contig from the tip of
DEFINITION the short arm of chromosome 16, spanning 2Mb of 16p13.3.
ACCESSION  Z84722
NID        g1817579
KEYWORDS   16p13.3.
SOURCE     human.
ORGANISM   Homo sapiens
REFERENCE  Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 19226)
AUTHORS    Flint, J. and Higgs, D.R.
TITLE      Direct Submission
JOURNAL    Submitted (28-JAN-1997) Sanger Centre, 970124/Hinxton,
Cambridgeshire, CB10 1RQ, UK. E-mail enquiries: humpub@sanger.ac.uk
COMMENT    IMPORTANT: This sequence is not the entire insert of clone GG4.
This clone was sequenced at the Institute of Molecular Medicine.
The true left end of clone GG4 is at 1 in this sequence. The true
right end of clone RA36 is at 456.
The true left end of clone PX94 is at 19090.
GG4 is from a 280kb clone contig extending from the telomere of
16p.
Higgs D.R., Flint J. unpublished. MRC Molecular Haematology Unit,
Institute of Molecular Medicine, Oxford.
GG4 came from the Los Alamos, flow sorted human Chromosome 16
library.

FEATURES
source      Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
/map="16p13.3"
/clone="GG4"
601..894
/note="AluJb repeat: matches 301..5 of consensus"
1156..1290
/note="Alusx repeat: matches 1..136 of consensus;
incomplete repeat"
1291..1601
/note="Alusg repeat: matches 1..300 of consensus"
1602..1758
/note="Alusg repeat: matches 132..288 of consensus;
incomplete repeat"
3487..3784
/note="Alusg repeat: matches 1..299 of consensus"
3809..4104

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repeat_region
repeat_region
repeat_region
repeat_region
repeat_region

Query Match      98.9%; Score 145.4; DB 11; Length 19226;
Best Local Similarity 99.3%; Pred. No. 9.1e-38;
Matches 146; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 agataactgggccaacatgactcagctctctggaggccaacagagctctgagtcac 60
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QY 61 ctgtgggggtggagtgagggaaggaagggtggaatgctgctgattacaacctct 120
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Db 11123 CTGTGGGGTGGAGTGGGACAAGGAAGGGTGAATGCTGCTGATTACACCTCT 11182
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QY 121 ggtgctgcctccctcctcttattct 147
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Db 11183 GGTGCTGCCTCCCTCCTCTGTTATCT 11209
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BASE COUNT      5242 a   4881 c   4603 g   4500 t
ORIGIN

Query Match      98.9%; Score 145.4; DB 11; Length 19226;
Best Local Similarity 99.3%; Pred. No. 9.1e-38;
Matches 146; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

/note="AluJo repeat: matches 1..302 of consensus"
4823..5030
/note="Alusg repeat: matches 2..208 of consensus;
incomplete repeat"
5053..5092
/note="20 copies of 2 mer 85 % conserved"
5122..5280
/note="FAM repeat: matches 164..5 of consensus"
5759..5903
/note="L1MC2 repeat: matches 169..321 of consensus"
6130..6427
/note="Alusg repeat: matches 297..1 of consensus"
6428..6724
/note="AluJo repeat: matches 299..1 of consensus"
7144..7265
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7433..7747
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16585..16668))
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8094..8307
/note="Alusg repeat: matches 212..1 of consensus;
incomplete repeat"
8578..8861
/note="AluY repeat: matches 3..297 of consensus"
8907..9210
/note="AluJb repeat: matches 300..1 of consensus"
9807..9887
/note="MIR repeat: matches 105..185 of consensus"
12438..12731
/note="AluJb repeat: matches 297..3 of consensus"
12946..13243
/note="Alusg repeat: matches 299..2 of consensus"
14000..14139
/note="AluJb repeat: matches 2..141 of consensus;
incomplete repeat"
14140..14453
/note="Alusx repeat: matches 1..302 of consensus"
14454..14596
/note="L1MB6 repeat: matches 760..907 of consensus"
16385..16584
/note="10 copies of 20 mer 91 % conserved"
18800..19089
/note="Alusx repeat: matches 1..293 of consensus"

BASE COUNT      5242 a   4881 c   4603 g   4500 t
ORIGIN
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S49899 356 bp DNA PRI 10-JUL-1992  
 LOCUS alpha-globin gene cluster: {5' region, major regulatory element}  
 DEFINITION [human, Genomic, 356 nt].  
 S49899  
 NID 9233777  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE 1 (bases 1 to 356)  
 AUTHORS Jarman A.P., Wood, W.G., Sharpe, J.A., Gourdon, G., Ayyub, H. and  
 Higgs, D.R.  
 TITLE Characterization of the major regulatory element upstream of the  
 human alpha-globin gene cluster  
 JOURNAL Mol. Cell. Biol. 11 (9), 4679-4689 (1991)  
 MEDLINE 91342671  
 REMARK GenBank staff at the National Library of Medicine created this  
 entry [NCBI g1bbsq 49899] from the original journal article.  
 COMMENT This sequence comes from fig 5.  
 REGION: alpha-globin gene cluster.  
 FEATURES  
 source 1..356  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 BASE COUNT 89 a 89 c 108 g 70 t  
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 Best Local Similarity 99.3%; Pred. No. 7.4e-38;  
 Matches 146; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 agataactgggccaacatgactgcttctggaggccaacagactctgagtcac 60  
 Db 111 AGATAACTGGCCCAACCATGACTGCTCTGGAGGCCACAGGACTCTGAGTCATC 170

Qy 61 ctgtgggggtggaggtgggacaagggaagggtgaatgctgctgattacaacctct 120  
 Db 171 CTGTGGGGGTGGAGGTGGGCAAGGAAGGGGTGAATGCTGCTGATTACAACCTCT 230

Qy 121 ggtgctgctccctccctcttattct 147  
 Db 231 GGTCCTCCCTCCCTCCCTCTCTTATCT 257

RESULT 4  
 HSGG4  
 LOCUS  
 DEFINITION Human DNA sequence from cosmid GG4 from a contig from the tip of  
 the short arm of chromosome 16, spanning 2Mb of 16p13.3.  
 S49899  
 NID 91817579  
 KEYWORDS 16p13.3  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE 1 (bases 1 to 19226)  
 AUTHORS Flint, J. and Higgs, D.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-JAN-1997) Sanger Centre, 970124/Hinxton,  
 Cambridgeshire, CB10 1RQ, UK. E-mail enquires: humpbesanger.ac.uk  
 IMPORTANT: This sequence is not the entire insert of clone GG4.  
 This clone was sequenced at the Institute of Molecular Medicine.  
 The true left end of clone GG4 is at 1 in this sequence. The true  
 right end of clone R336 is at 456.  
 The true left end of clone PX94 is at 19090.  
 GG4 is from a 280kb clone contig extending from the telomere of  
 16p.  
 Higgs D.R., Flint J. unpublished. MRC Molecular Haematology Unit,  
 Institute of Molecular Medicine, Oxford.

GG4 came from the Los Alamos, flow sorted human Chromosome 16  
 library.  
 FEATURES  
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 1156..1290  
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 incomplete repeat"  
 1291..1601  
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 1602..1758  
 /note="AluSg repeat: matches 132..288 of consensus;  
 incomplete repeat"  
 3487..3784  
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 incomplete repeat"  
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 5122..5280  
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 /note="AluSp repeat: matches 1..303 of consensus"  
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 12438..12731  
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 incomplete repeat"  
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 14454..14596  
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 16385..16584  
 /note="10 copies of 20 mer 91 & conserved"  
 18800..19089  
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BASE COUNT	5242 a	4881 c	4603 g	4500 t
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Query Match	98.9%;	Score 145.4;	DB 41;	Length 19226;
Best Local Similarity	99.3%;	Pred. No. 9.1e-38;		
Matches 146;	Conservative	0;	Mismatches 1;	Indels 0;
Gaps	0;			
QY	1	agataactgggccaacactgactcagctgttcttgaggccaacagagctcttgagtcac	60	
DB	11063	AGATAACTGGGCCAACCACTGACTCAGTGTCTTGAGGCCACAGAGCTGCTGAGTCATC	11122	
QY	61	ctgtgggggtggaggtgggacaagggaagggtgaatggtactctgattacaacctct	120	
DB	11123	CTGTGGGGTGGAGTGGGACAGAGGGAAGGGTGAATGGTACTGCTGATTACACCTCT	11182	
QY	121	ggtgctgctccctcctctgtttatct	147	
DB	11183	GGTGTGCTCCCTCCCTCTGTTTATCT	11209	
RESULT	5			
S78508				
LOCUS	277 bp	DNA	ROD	26-SEP-1995
DEFINITION	alpha globin (regulatory element)			[mice, Genomic, 277 nt].
ACCESSION	S78508			
NID	999308			
KEYWORDS	Mus sp.			
SOURCE	Mus sp.			
ORGANISM	Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1 (bases 1 to 277)			
AUTHORS	Gourdon, G., Sharpe, J.A., Higgs, D.R. and Wood, W.G.			
TITLE	The mouse alpha-globin locus regulatory element			
JOURNAL	Blood 86 (2), 766-775 (1995)			
MDLINE	95329736			
REMARK	GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 168417] from the original journal article. This sequence comes from Fig. 2B.			
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DB	171	CTTGGGGGTACAGAGTCAGAAA---GGAAAGGACAAATGGTACCACCTGATTAGGACCTCT	227	
QY	121	ggtgctgctccctcctctgtttatct	147	
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LOCUS	330 bp	DNA	ROD	29-NOV-1995
DEFINITION	Mus musculus C57BL/alpha-globin locus control region.			

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Genomics 41 (2), 236-242 (1997)  
MEDLINE 97288521  
REFERENCE 2 (bases 1 to 9750)  
AUTHORS Olson, P.  
TITLE Direct Submission  
JOURNAL Submitted (09-OCT-1996) Cutaneous Biology Research Center,  
Massachusetts General Hospital, Third floor, Bldg. 149, Thirteenth  
St., Charlestown, MA 02129, USA  
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LQVANLPKGGNLTGALNFIRQNFRTQAGNRPARKIGVILITDGSDDDVEAPS  
KKLKDGEVLEAIGKNADEVELMIATDPDTHYVADFSLRIVDDTLINLCS  
VKGPDLEAPNLVISERTHSRFSVTPPSDSVDYKVEIYVSGGKROEFTYSRME  
TSTVLKDLKPTETVYVYVVEDEYSEPLKTEKTLFVPSVNLINIDYPTTMHYQW  
QPVGATGYLSKPKVKDTEPRKEVRLGPTVNDMOLTDLPNTVAVTVQVLAHDL  
TSEPTVREVTPLPRQDLKRDVTHSTNNVFEVPVGVKRVIVRYKTPEDVKEV  
EVDRESSTSLKDLFSLQTLVSVSAVDGESPPVTAQETTRPVAPNLIKTEVTS  
EGFRGDSHSDLSLXILTWGPRGSDKMETILNGENTLNFENLNPNTIIEVSTIA  
IYADESDHDLIGSERTPLITLQAPKSGPRNQVYVYVNSLTVNPDVPSAGRVQKIR  
ITYQPTSGEHEQTTIGGRNSVLAQLKPDPTTYTIVSSLYPDGEGRMTRGRTK  
PLUNTRNLRVNDPSTSLNVRWDAEGRNQYKLFYAPAAAGPEELVYIPGNTNYAIL  
RNLPQDTVYTVTVVTEGDDGTSDTGRTLMRGLARNVQVYVYVNPRLVSGDGPAP  
GNLPQTVYVSPVDTGRPSYVVPNTVMVHLERLPDLTLYSNVLVYVSDGNGPS  
PQAQRTLRSPGRNLRVGEENTSLVANDHAGDPVQOYRIIYSPVGDPIDEYTVV  
GRNNVILQPDPTPYKTIIVATEDGGLTGNGRTVGLLPQNNIISDNDVTRF  
RWSDPSPSPVLGYKIVYKPVSGNEPMEFVGMTSYLNLNMPSTIYDYNVAQYDS  
GLSVPLTQGTLLXNLVTLQYIGWDTFCVKSHPRAATSYRLKSPADGTRGEEI  
TVRGSETSGCTGLSPDPTGYTVQTPNLEGVGSVKEHTVTKTEAPETPTPPP  
PTIIPARDVKAKADIVFLTDSASIGDNNKVKVFKFNTVGGFDEISPAQIOVS  
FVQYSDVKSEKFLNTKDALGALQNIYRGNTRTGKALTFFKEKVLTWESGMR  
KNPKVLVYVDTGRSDQVKKALVYIQQSGFSVYVGVADVYNELANLASKPSEHY  
FVDDPSEFKEDNLTIVCEATSSCPILYLDGTPSPGKMLEATNLNTEKNFASVQ  
GVSLSEGSFSPSYVRIQKNFVQNPADLHPLGPPSYTIIILLFLPTPTSPFAI  
WQITDRDYKPVQGVIAVDPSSKTLSTFFNNDTRGEVQTVTFDTEEVKTLFGSFFKHVH

mat\_peptide 186. .9302  
/gene="COL12A1"  
/note="member of the FACIT group of collagens"  
/product="collagen type XII alpha-1"  
9306. 9750  
/gene="COL12A1"  
BASE COUNT 2885 a 2150 c 2372 g 2343 t  
ORIGIN

Query Match 21.1%; Score 31; DB 12; Length 9750;  
Best Local Similarity 56.1%; Pred. No. 3.4;  
Matches 78; Conservative 0; Mismatches 60; Indels 1; Gaps 1;  
QY 5 aactggggcccaaccatgactcagtcgtcttctggaggccaacaggactctctgagtcactcgt 64  
Db 8987 ACCTGGGCTGGGGGGGGCCAGGCTTCCGGGGCACACACAGGAGTGCAGGACCTCGGG 9046  
QY 65 ggggggtggagtgaggacagggaagggtgaatggtaact-gctgattacaacctgtgt 123  
Db 9047 GGAACGAGGTTTGGCAGAGAGAAAGGTAAGAGGGGTACTGGATCTCTCAGGACCTCGGG 9106  
QY 124 gctgctccccctcctctgt 142  
Db 9107 GCTGCTGGGCCCCAGCT 9125

RESULT 8  
HSU1  
LOCUS Human collagen type XII alpha-1 precursor (COL12A1) mRNA, complete cds.  
DEFINITION  
ACCESSION U73778  
NID 91846004  
KEYWORDS i of 2  
SEGMENT human.  
SOURCE  
ORGANISM Homo sapiens  
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;  
Homo.  
REFERENCE 1 (bases 1 to 9750)  
AUTHORS Gerecke, D.R., Olson, P.F., Koch, M., Knoll, J.H., Taylor, R.,  
Hudson, D.L., Champilaud, M.F., Olsen, B.R. and Burgeson, R.E.  
TITLE Complete primary structure of two splice variants of collagen XII,  
and assignment of alpha 1(XII) collagen (COL12A1), alpha 1(XIX)  
collagen (COL9A1), and alpha 1(XIX) collagen (COL19A1) to human  
chromosome 6q12-q13  
JOURNAL Genomics 41 (2), 236-242 (1997)  
MEDLINE 97288521  
REFERENCE 2 (bases 1 to 9750)  
AUTHORS Olson, P.  
TITLE Direct Submission  
JOURNAL Submitted (09-OCT-1996) Cutaneous Biology Research Center,  
Massachusetts General Hospital, Third floor, Bldg. 149, Thirteenth  
St., Charlestown, MA 02129, USA  
Location/Qualifiers  
1. .9750  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="6"  
/cell\_type="primary foreskin fibroblasts; primary foreskin  
keratinocytes; squamous cell carcinoma cells; endothelial  
(HUVEC) cell lines"  
1. .113

5'UTR  
sig\_peptide  
CDS



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RESULT 10
HSPKCG5      1149 bp      DNA      PRI      08-AUG-1995
LOCUS        H.sapiens gene for protein kinase C gamma, upstream region.
DEFINITION   X62533
ACCESSION    X62533
NID          935498
KEYWORDS     protein kinase C; serine/threonine protein kinase.
SOURCE       human.
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 1149)
AUTHORS      Mahajna,J., King,P., Parker,P. and Haley,J.
TITLE        Autoregulation of cloned human protein kinase C beta and gamma gene
JOURNAL      DNA Cell Biol. 14 (3), 213-222 (1995)
MEDLINE      95186059
REFERENCE    2 (bases 1 to 1149)
AUTHORS      Haley,J.D.
TITLE        Direct Submission
JOURNAL      Submitted (12-JUL-1990) J.D. Haley, ONCOGENE SCIENCE INC., 350
COMMUNITY DRIVE, MANHASSET, NY 11030, USA
FEATURES     source
             1..1149
             /organism="Homo sapiens"
             /db_xref="taxon:9606"
             /cell_type="leukocyte"
             /clone.lib="lambda gt10"
             /chromosome="16"
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             /gene="PKC-G"
             1147..>1149
             /gene="PKC-G"
             /codon_start=1
             /product="protein kinase C gamma"
BASE COUNT   296 a 331 c 363 g 159 t
ORIGIN
Query Match      20.8%; Score 30.6; DB 40; Length 1149;
Best Local Similarity 58.5%; Pred. No. 4.1;
Matches 72; Conservative 0; Mismatches 49; Indels 2; Gaps 1;

QY 20 gactcagtcctctggaggccaacgagctctgtgagtcactctgtgggggtggaggtggg 79
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 585 GACACAGGACCCAGGCGGCCGCCACAGGACACACAGGACGACCTAGTGGGGAGGAACGCG 644
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 80 acaagggaaagggtgaatgctactgctgatta--caacctctgtgctgctccctc 137
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 645 GCAGGATGACAGATTCAGGGTGTGGGGGGAGCCAGGCTCAGAGATGCCCTCCCTC 704
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 138 ctg 140
|||
Db 705 CAG 707

RESULT 11
AC003112
LOCUS        Human DNA from chromosome 19 specific cosmid R30292, genomic
DEFINITION   sequence, complete sequence.
ACCESSION    AC003112
NID          g2636669
KEYWORDS     HTG.
SOURCE       human.
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 40668)
AUTHORS      Lamerdin,J.E., McCready,P.M., Adamson,A.W., Burkhardt-Schultz,K.,
Gordon,L., Christensen,M., Kyle,A., Ramirez,M., Stillwagen,S.,
Garnes,J., Danganan,L., Bruce,R., Quan,G., Montgomery,M., Ow,D.,
Kobayashi,A., Olsen,A.O. and Carrano,A.V.
TITLE        Sequence analysis of an -1 Mb region containing the MEF2B gene in
19p12
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 40668)
AUTHORS      Lamerdin,J.E.
TITLE        Direct Submission
JOURNAL      Submitted (21-NOV-1997) Human Genome Center, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
FEATURES     source
             1..40668
             /organism="Homo sapiens"
             /db_xref="taxon:9606"
             /clone="R30292"
             /chromosome="19"
             /map="19p12 between UBA52 and D19S451"
             /cell_line="5HL2-B"
             /clone.lib="LL19NC03 R chromosome 19 cosmid library"
             /note="LL19NC03 cosmid library constructed at LLNL from
flow-sorted chromosomes from hybrid 5HL2-B, which carries
chromosome 19 as its only human chromosome."
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frame: 1, quality: good, score: 71.000"
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             /note="predicted exon, program: grail2exons_human_1.3,
frame: 1, quality: good, score: 62.000"
             2257..8516
             /standard_name="endogenous retroviral sequence"
             /note="HERV9 retroviral sequence"
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             /rpt_family="Alu"
             5425..5722
             /rpt_family="Alu"
             complement(6486..6772)
             /rpt_family="Alu"
             complement(7505..7783)
             /rpt_family="Alu"
             8951..9254
             /rpt_family="Alu"
             9358..9535
             /rpt_family="LTR12"
             complement(9445..9505)
             /note="predicted exon, program: grail2exons_human_1.3,
frame: 1, quality: good, score: 63.000"
             complement(9629..9672)
             /note="predicted exon, program: grail2exons_human_1.3,
frame: 1, quality: excellent, score: 75.000"
             complement(9928..10123)
             /rpt_family="Alu"
             10409..10548
             /note="DDS similarity to AA047548 zf15e02.r1 Soares fetal
heart NBH19W Homo sapiens cDNA clone 377018 5' (1..138);
96% identity.--Other overlapping matches:--(10435..10548)
DDS similarity to AA136115 zk90b04.r1 Soares pregnant
uterus NBHPU Homo sapiens cDNA clone 490063 5' (1..110);
93% identity.--(10466..10548) DDS similarity to AA452628
zx33f04.r1 Soares total fetus NB2HF8 9w Homo sapiens cDNA
clone 788287 5' (1..82); 95% identity.--(10486..10548) DDS
similarity to AA009412 ze82h02.r1 Soares fetal heart
NBH19W Homo sapiens cDNA clone 365523 5' (1..61); 97%
identity."
             10643..10725
             /note="predicted exon, program: grail2exons_human_1.3,
frame: 1, quality: excellent, score: 100.000--DDS
similarity to AA047548 zf15e02.r1 Soares fetal heart
NBH19W Homo sapiens cDNA clone 377018 5' (139..221); 100%
identity.--DDS similarity to AA136115 zk90b04.r1 Soares
pregnant uterus NBHPU Homo sapiens cDNA clone 490063 5'
(111..192); 99% identity.--DDS similarity to AA452628
zx33f04.r1 Soares total fetus NB2HF8 9w Homo sapiens cDNA
clone 788287 5' (83..165); 100% identity.--DDS similarity

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to AA009412 ze82h02.r1 Soares fetal heart NBHH19W Homo
sapiens cDNA clone 365523 5' (62. .144); 100% identity."
11127. .11331
/notes="DDS similarity to AAL36115 zk90b04.r1 Soares
pregnant uterus NBHPU Homo sapiens cDNA clone 490063 5'
(193. .394); 94% identity.--DDS similarity to AA009412
ze82h02.r1 Soares fetal heart NBHH19W Homo sapiens cDNA
clone 365523 5' (145. .346); 96% identity.--(1121. .11331)
DDS similarity to AA009693 ze82h02.s1 Soares fetal heart
NBHH19W Homo sapiens cDNA clone 365523 3' (429. .307); 95%
identity.--(11127. .11246) DDS similarity to AA047548
zf1se02.r1 Soares fetal heart NBHH19W Homo sapiens cDNA
clone 377018 5' (222. .341); 97% identity.--(11061. .11331)
predicted exon, program: graill2exons_human_1.3, frame: 0,
quality: good, score: 73.000--(11061. .11209) DDS
similarity to AA452628 zx33f04.r1 Soares total fetus
NB2HF8 9w Homo sapiens cDNA clone 788287 5' (167. .313);
98% identity."
complement(11869. .12161)
/rpt_family="Alu"
12502. .12581
/notes="DDS similarity to AAL36115 zk90b04.r1 Soares
pregnant uterus NBHPU Homo sapiens cDNA clone 490063 5'
(395. .477); 92% identity.--DDS similarity to AA009412
ze82h02.r1 Soares fetal heart NBHH19W Homo sapiens cDNA
clone 365523 5' (347. .427); 94% identity.--DDS similarity
to AA009693 ze82h02.s1 Soares fetal heart NBHH19W Homo
sapiens cDNA clone 365523 3' (306. .228); 99%
identity.--DDS similarity to AA450010 zx33f04.s1 Soares
total fetus NB2HF8 9w Homo sapiens cDNA clone 788287 3'
(309. .229); 99% identity.--"
complement(12966. .13240)
/rpt_family="Alu"
complement(13274. .13531)
/rpt_family="Alu"
complement(13756. .14029)
/notes="predicted exon, program: graill2exons_human_1.3,
frame: 2, quality: good, score: 61.000--Other overlapping
matches.--(13756. .13826) DDS similarity to AA009412
ze82h02.r1 Soares fetal heart NBHH19W Homo sapiens cDNA
clone 365523 5' (428. .496); 97% identity.--(13756. .13984)
DDS similarity to AA009693 ze82h02.s1 Soares fetal heart
NBHH19W Homo sapiens cDNA clone 365523 3' (227. .1); 98%
identity.--(13756. .13984) DDS similarity to AA450010
zx33f04.s1 Soares total fetus NB2HF8 9w Homo sapiens cDNA
clone 788287 3' (228. .1); 99% identity.--"
complement(14100. .14672)
/rpt_family="Alu"
14885. .15317
/notes="DDS similarity to AA406406 zvllie07.s1 Soares NBHMPu
S1 Homo sapiens cDNA clone 753348 3' (1. .433); score: 858
identity: 431/433 (99%).--(14884. .15237) DDS similarity
to W37175 zb21a02.r1 Soares fetal lung NBHL19W Homo
sapiens cDNA clone 302666 5' (1. .355); 94%
identity.--(15227. .14885) DDS similarity to AAL21532
zk89c11.s1 Soares pregnant uterus NBHPU Homo sapiens cDNA
clone 490004 3' (342. .1); 99% identity.--(15227. .14885)
DDS similarity to AAL27694 zk89c11.r1 Soares pregnant
uterus NBHPU Homo sapiens cDNA clone 490004 5' (126. .467);
99% identity.--(15227. .14897) DDS similarity to W46603
zc32h10.r1 Soares senescent fibroblasts NBHSF Homo sapiens
cDNA clone 324067 5' (328. .1); 98%
identity.--(15227. .15088) DDS similarity to W46604
zc32h10.s1 Soares senescent fibroblasts NBHSF Homo sapiens
cDNA clone 324067 3' (322. .465); 96% identity."
15713. .15760
/notes="DDS similarity to AAL21532 zk89c11.s1 Soares
pregnant uterus NBHPU Homo sapiens cDNA clone 490004 3'
(389. .343); 99% identity.--DDS similarity to AAL27694
zk89c11.r1 Soares pregnant uterus NBHPU Homo sapiens cDNA
clone 490004 5' (77. .125); 90% identity.--(15735. .15713)
DDS similarity to W46603 zc32h10.r1 Soares senescent
fibroblasts NBHSF Homo sapiens cDNA clone 324067 5'

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(351. .329); 100% identity.--(15735. .15713) DDS similarity
to W46604 zc32h10.s1 Soares senescent fibroblasts NBHSF
Homo sapiens cDNA clone 324067 3' (299. .321); 100%
identity."
complement(15895. .16082)
/notes="predicted exon, program: graill2exons_human_1.3,
frame: 0, quality: excellent, score: 81.000--Other
overlapping matches.--(15936. .15895) DDS similarity to
AAL21532 zk89c11.s1 Soares pregnant uterus NBHPU Homo
sapiens cDNA clone 490004 3' (431. .390); 100%
identity.--(15970. .15895) DDS similarity to AAL27694
zk89c11.r1 Soares pregnant uterus NBHPU Homo sapiens cDNA
clone 490004 5' (1. .76); 100% identity."
17926. .18190
/rpt_family="Alu"
complement(18270. .18438)
/notes="predicted exon, program: graill2exons_human_1.3,
frame: 0, quality: excellent, score:
100.000--(18438. .18284) DDS similarity to W66776
mel7b11.r1 Soares mouse embryo NBME13.5 14.5 Mus musculus
cDNA clone 387741 5' similar to PIR:B38252 B38252
granulocyte colony-stimulating factor precursor
(157. .1); 82% identity.--(18438. .18406) DDS similarity to
AA049280 mj45d02.r1 Soares mouse embryo NBME13.5 14.5 Mus
musculus cDNA clone 479043 5' similar to SW:IL6B-MOUSE
Q00560 INTERLEUKIN-6 RECEPTOR BETA PRECURSOR (432. .464);
88% identity."
complement(18540. .18697)
/notes="predicted exon, program: graill2exons_human_1.3,
frame: 1, quality: excellent, score: 100.000--DDS
similarity to W66776 mel7b11.r1 Soares mouse embryo
NBME13.5 14.5 Mus musculus cDNA clone 387741 5' similar to
PIR:B38252 B38252 granulocyte colony-stimulating factor
receptor precursor (316. .158); 92% identity.--DDS
similarity to AA049280 mj45d02.r1 Soares mouse embryo
NBME13.5 14.5 Mus musculus cDNA clone 479043 5' similar to
SW:IL6B-MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN
PRECURSOR (274. .431); 93% identity.--"
complement(19080. .19379)
/rpt_family="Alu"
complement(20080. .20249)
/notes="predicted exon, program: graill2exons_human_1.3,
frame: 2, quality: excellent, score: 100.000--DDS
similarity to AA049280 mj45d02.r1 Soares mouse embryo
NBME13.5 14.5 Mus musculus cDNA clone 479043 5' similar to
SW:IL6B-MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN
PRECURSOR (104. .273); 86% identity.--(20245. .20080) DDS
similarity to W66776 mel7b11.r1 Soares mouse embryo
NBME13.5 14.5 Mus musculus cDNA clone 387741 5' similar to
PIR:B38252 B38252 granulocyte colony-stimulating factor
receptor precursor (482. .317); 86% identity."
complement(20420. .20549)
/notes="predicted exon, program: graill2exons_human_1.3,
frame: 0, quality: excellent, score:
100.000--(20522. .20420) DDS similarity to AA049280
mj45d02.r1 Soares mouse embryo NBME13.5 14.5 Mus musculus
cDNA clone 479043 5' similar to SW:IL6B-MOUSE Q00560
INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (-1. .103); 85%
identity.--(20549. .20479) DDS similarity to AA042914
zk56f01.s1 Soares pregnant uterus NBHPU Homo sapiens cDNA
clone 486841 3' (338. .410); 96% identity.--"
complement(20779. .21043)
/rpt_family="Alu"
complement(21209. .21494)
/notes="predicted exon, program: graill2exons_human_1.3,
frame: 0, quality: excellent, score: 94.000--Other
overlapping matches.--(21494. .21213) DDS similarity to
AA042914 zk56f01.s1 Soares pregnant uterus NBHPU Homo
sapiens cDNA clone 486841 3' (55. .337); 99%
identity.--(21362. .21268) DDS similarity to W46603
zc32h10.r1 Soares senescent fibroblasts NBHSF Homo sapiens
cDNA clone 324067 5' (448. .352); 97%
identity.--(21494. .21268) DDS similarity to W46604

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zc32h10.s1 Soares senescent fibroblasts NBHSF Homo sapiens
cDNA clone 59425 3' (73. .298); 99% identity."
complement(21854. .22765)
/rpt_family="Alu"
repeat_region
complement(22928. .23336)
/rpt_family="Alu"
repeat_region
23983. .24280
/rpt_family="Alu"
repeat_region
complement(24432. .24658)
/rpt_family="Alu"
repeat_region
complement(32650. .32696)
/rpt_family="Alu"
misc_feature
frame: 0, quality: good, score: 74.000"
/note="predicted exon, program: grill2exons_human_1.3,
34712. .34777
/note="predicted exon, program: grill2exons_human_1.3,
frame: 1, quality: good, score: 69.000"
/note="predicted exon, program: grill2exons_human_1.3,
35520. .35664
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frame: 2, quality: excellent, score: 100.000--Other
overlapping matches--(35559. .35664) DDS similarity to
R59871 yH07c12.r1 Homo sapiens cDNA clone 42571 5'
(1. .107); 94% identity.--(35575. .35664) DDS similarity to
R89669 ym37f05.r1 Homo sapiens cDNA clone 166881 5'
(1. .90); 100% identity."
35752. .35843
/note="predicted exon, program: grill2exons_human_1.3,
frame: 2, quality: excellent, score: 98.000--DDS
similarity to 59871 yH07c12.r1 Homo sapiens cDNA clone
42571 5' (108. .199); 97% identity.--DDS similarity to
R89669 ym37f05.r1 Homo sapiens cDNA clone 166881 5',
(91. .181); 97% identity.--DDS similarity to N99345
IMAGE:59425 Homo sapiens cDNA clone 59425 (17. .111); 100%
identity."
complement(36643. .36920)
/rpt_family="Alu"
repeat_region
complement(37271. .37547)
/rpt_family="Alu"
misc_feature
37623. .37775
/note="predicted exon, program: grill2exons_human_1.3,
frame: 2, quality: good, score: 65.000--DDS similarity to
59871 yH07c12.r1 Homo sapiens cDNA clone 42571 5',
(200. .353); 99% identity.--DDS similarity to R99669
ym37f05.r1 Homo sapiens cDNA clone 166881 5' (182. .337);
98% identity.--DDS similarity to N99345 IMAGE:59425 Homo
sapiens cDNA clone 59425 (112. .264); 100%
identity.--(37624. .37775) DDS similarity to AA424113
zv80e08.r1 Soares total fetus NB2HF8 9w Homo sapiens cDNA
clone 759974 5' (1. .152); 99% identity."
complement(38029. .38339)
/rpt_family="Alu"
repeat_region
38648. .38750
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frame: 1, quality: excellent, score: 84.000--DDS
similarity to N99345 IMAGE:59425 Homo sapiens cDNA clone
59425 (265. .363); 96% identity.--DDS similarity to
AA424113 zv80e08.r1 Soares total fetus NB2HF8 9w Homo
sapiens cDNA clone 759974 5' (153. .254); 99%
identity.--DDS similarity to AA378559 EST91296 Synovial
sarcoma Homo sapiens cDNA 5' end (23. .124); 100%
identity."
39803. .39920
/note="DDS similarity to N99345 IMAGE:59425 Homo sapiens
cDNA clone 59425 (384. .480); 99% identity.--DDS similarity
to AA378559 EST91296 Synovial sarcoma Homo sapiens cDNA 5'
end (125. .242); 100% identity.--(39812. .39941) predicted
exon, program: grill2exons_human_1.3, frame: 0, quality:
excellent, score: 94.000--(39870. .39870) DDS similarity to
AA424113 zv80e08.r1 Soares total fetus NB2HF8 9w Homo
sapiens cDNA clone 759974 5' (255. .322); 100% identity."
40023. .40140
/note="DDS similarity to N99345 IMAGE:59425 Homo sapiens
cDNA clone 59425 (481. .598); 100% identity.--DDS
similarity to AA378559 EST91296 Synovial sarcoma Homo

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sapiens cDNA 5' end (243. .308); 94%
identity.--(40023. .40102) DS similarity to AA424113
zv80e08.r1 Soares total fetus NB2HF8 9w Homo sapiens cDNA
clone 759974 5' (323. .402); 100% identity.--(40081. .40140)
predicted exon, program: grill2exons_human_1.3, frame: 0,
quality: marginal, score: 44.000"
complement(40353. .40657)
repeat_region
BASE COUNT 8422 a 12040 c 11050 g 9156 t
ORIGIN

Query Match 20.7%; Score 30.4; DB 11; Length 40568;
Best Local Similarity 55.6%; Pred. No. 5.8;
Matches 58; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 27 tgctctggaggccacaggaactcttgatcctcgtgggtgagtggtggagtggaagg 86
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 34851 TTCTCTGGATGACACAGGAGACTTTGCTGGGGGTGTCGTGGGAGTGGGGTCGGG 34910
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 87 aaagggtggaatggtactgtctgattacaacctctctgctgctgctc 130
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 34911 AATGGGAGATCTCTCCAGTAGTGTGACGGGCTGGGGTTCCTCT 34954

RESULT 12
AC003991/c
LOCUS AC003991 118313 bp DNA PRI 14-JAN-1998
DEFINITION Human BAC clone RG167B05 from 7q21, complete sequence.
ACCESSION AC003991
NID G2772535
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 118313)
Murray, J, Rohlfing, T and Antoniou, B.
The sequence of H. sapiens BAC clone RG167B05
Unpublished (1998)
REFERENCE 2 (bases 1 to 118313)
Waterston, R.
Direct Submission
Submitted (14-JAN-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
SUBMITTED BY:
Genome Sequencing Center
Department of Genetics
Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:sapiens@watson.wustl.edu

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded or sequenced with an alternate
chemistry; an attempt was made to resolve all sequencing problems,
such as compressions and repeats; all regions were covered by
sequence from more than one subclone; and the assembly was
confirmed by restriction digest.

MAPPING INFORMATION:
The sequence of this clone was established as part of a mapping and
sequencing collaboration between the NHGRI Chromosome 7 Mapping
Project (Eric D. Green, Director), John D. McPherson in the
Department of Genetics (Washington University), and the Washington
University Genome Sequencing Center. For additional information
about the map position of this sequence, see
http://www.nhgri.nih.gov/DIR/GTB/CHR7 or send

```

mailto:egreen@hgrl.nih.gov

#### SOURCE INFORMATION:

Clone RG167B05 is from the first release of the human BAC library C17B-978SK-B. The library contains cloned DNA from the male fibroblast cell line 978SK. See: Shizuwa et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). This clone is available from Research Genetics, Inc. (<http://www.resgen.com>).

VECTOR: pBelOBAc11

Selection: chloramphenicol

#### NEIGHBORING SEQUENCE INFORMATION:

The actual start of this clone is at base position 1 of RG167B05. actual end of this clone is at base position 118313 of RG167B05.

This clone contains STS SWS2908 (NID:g1113638).

#### FEATURES

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	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/chromosome="7"
	/clone="RG167B05"
	/clone_lib="C17B-978SK-B"
	/map="7q21"
	353..519
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repeat_region	527..626
repeat_region	/rpt_family="MER1_type"
repeat_region	686..832
repeat_region	/rpt_family="MER1_type"
repeat_region	914..999
repeat_region	/rpt_family="L2"
repeat_region	1073..1117
repeat_region	/rpt_family="L2"
repeat_region	1359..1503
repeat_region	/rpt_family="L2"
repeat_region	3917..4205
repeat_region	/rpt_family="Alu"
repeat_region	4701..4865
repeat_region	/rpt_family="Alu"
gene	complement(5050..7954)
CDS	/gene="SRI"
	/note="match to sorcin protein P30626 (PID:g267021); H_RG167B05.1"
	/codon_start=1
	/product="calcium binding protein amplified in mutlidrug-resistant cells"
	/db_xref="PID:g2772536"
	/translation="MAYPHGAGGGYYPGGYGAGGAPPGQTQDPLYGYFAAVAG ODGQIDADELQRLTQSGIAGYK"
repeat_region	9625..10516
repeat_region	/rpt_family="L1"
repeat_region	10518..11038
repeat_region	/rpt_family="L1"
repeat_region	11200..11288
repeat_region	/rpt_family="MIR"
repeat_region	11353..11404
repeat_region	/rpt_family="MER1_type"
repeat_region	11466..11711
repeat_region	/rpt_family="MER1_type"
repeat_region	12803..12813
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repeat_region	13488..13527
repeat_region	/rpt_family="MIR"
repeat_region	15273..15566
repeat_region	/rpt_family="Alu"
repeat_region	15767..15829
repeat_region	/rpt_family="MER1_type?"
repeat_region	15947..16238
repeat_region	/rpt_family="Alu"
repeat_region	16244..16326
repeat_region	/rpt_family="MER1_type?"
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repeat_region	/rpt_family="L1"
repeat_region	16912..17147
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repeat_region	17199..17400
repeat_region	/rpt_family="MaLR"
repeat_region	17401..17517
repeat_region	/rpt_family="MER1_type?"
repeat_region	18465..18536
repeat_region	/rpt_family="L1"
repeat_region	18644..18689
repeat_region	/rpt_family="(CA)n"
repeat_region	19101..19157
repeat_region	/rpt_family="MIR"
repeat_region	19436..20346
repeat_region	/rpt_family="L1"
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repeat_region	21425..21738
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repeat_region	21816..21903
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repeat_region	24950..25239
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repeat_region	25673..25862
repeat_region	/rpt_family="L1"
misc_feature	26008..26260
	/note="match to EST AA327226 (NID:g1979532)"
repeat_region	26261..26341
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misc_feature	26342..26414
repeat_region	26564..26742
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repeat_region	28496..28701
repeat_region	/rpt_family="Alu"
repeat_region	28961..29023
repeat_region	/rpt_family="(TGGGA)n"
repeat_region	29217..29523
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repeat_region	30548..30650
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repeat_region	32058..32121
repeat_region	/rpt_family="L1"
repeat_region	32134..32276
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repeat_region	33240..36502
repeat_region	/rpt_family="L1"
repeat_region	36503..36633
repeat_region	/rpt_family="Alu"
repeat_region	36634..37363
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repeat_region	37394..37548
repeat_region	/rpt_family="MaLR"
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repeat_region	38133..38265
repeat_region	/rpt_family="Alu"
repeat_region	38278..38556

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repeat_region /rpt_family="Alu"
repeat_region 38746. .40503
repeat_region /rpt_family="L1"
repeat_region 40507. .40560
repeat_region /rpt_family="L1"
repeat_region 40573. .40874
repeat_region /rpt_family="Alu"
repeat_region 40948. .41237
repeat_region /rpt_family="Alu"
repeat_region 41457. .42699
repeat_region /rpt_family="L1"
repeat_region 43683. .44216
repeat_region /rpt_family="L1"
repeat_region 44330. .44975
repeat_region /rpt_family="L1"
repeat_region 45663. .46301
repeat_region /rpt_family="L2"
repeat_region 46475. .46665
repeat_region /rpt_family="Alu"
repeat_region 46691. .46867
repeat_region /rpt_family="Alu"
repeat_region 46875. .47123
repeat_region /rpt_family="L2"
repeat_region 47148. .47453
repeat_region /rpt_family="Alu"
repeat_region 47465. .47723
repeat_region /rpt_family="L2"
repeat_region 48947. .49001
repeat_region /rpt_family="MIR"
repeat_region 49438. .49710
repeat_region /rpt_family="Alu"
repeat_region 50605. .50902
repeat_region /rpt_family="Alu"
repeat_region 50923. .51302
repeat_region /rpt_family="L1"
repeat_region 51531. .51683
repeat_region /rpt_family="MER1_type"
repeat_region 51858. .52279
repeat_region /rpt_family="L1"
repeat_region 52333. .52634
repeat_region /rpt_family="Alu"
repeat_region 52761. .53284
repeat_region /rpt_family="MER4-group"
repeat_region 53422. .54408
repeat_region /rpt_family="GVA"
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repeat_region /note="CpG island (8GC-72.8, o/e=0.70, #CpGs=95)"
repeat_region 56698. .56786
repeat_region /rpt_family="Retroviral"
repeat_region 57713. .57791
repeat_region /rpt_family="MIR"
repeat_region 58071. .58124
repeat_region /rpt_family="L1"
repeat_region 58849. .59127
repeat_region /rpt_family="L1"
misc_feature 59146. .59176
misc_feature /note="match to EST AA493281 (NID:g2223122) nh55d02.s1"
misc_feature complement(59155. .59314)
repeat_region /note="match to EST AA493281 (NID:g2223122) nh55d02.s1"
repeat_region 59317. .59874
repeat_region /rpt_family="L1"
repeat_region 60086. .60425
repeat_region /rpt_family="Retroviral"
repeat_region 60906. .61152
repeat_region /rpt_family="L1"
repeat_region 61996. .62213
repeat_region /rpt_family="MIR"
repeat_region 62445. .63016
repeat_region /rpt_family="MER4-group"
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misc_feature complement(64841. .64977)
misc_feature /note="match to EST R27235 (NID:g783370) yh53a03.r1"
misc_feature complement(64937. .65009)
misc_feature /note="match to EST R76842 (NID:g851474) y163c09.r1"
misc_feature complement(65019. .65370)
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repeat_region /rpt_family="Alu"
repeat_region 68196. .68360
repeat_region /rpt_family="MER1_type"
repeat_region 70076. .70373
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misc_feature /note="match to EST AA244027 (NID:g1874750) nc04a09.r1"
misc_feature complement(71252. .71561)
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repeat_region 73462. .73704
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repeat_region 73841. .73890
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repeat_region 73904. .74470
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repeat_region 77027. .77111
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repeat_region 78203. .78305
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repeat_region 78316. .78394
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repeat_region 79187. .79434
repeat_region /rpt_family="Alu"
repeat_region 80384. .81898
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repeat_region 82043. .82107
repeat_region /rpt_family="MER2_type"
repeat_region 82259. .82394
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repeat_region 83316. .83472
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repeat_region 83526. .83705
repeat_region /rpt_family="MER1_type"
repeat_region 85044. .85127
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repeat_region 85398. .85585
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repeat_region /rpt_family="MER2_type"
repeat_region 86395. .86438
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repeat_region 88133. .88402
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* 108143 109610: contig of 1468 bp in length
* 109611 109625: gap of unknown length
* 109626 111369: contig of 1744 bp in length
* 111370 111384: gap of unknown length
* 111385 113066: contig of 1682 bp in length
* 113067 113081: gap of unknown length
* 113082 114820: contig of 1739 bp in length
* 114821 114835: gap of unknown length
* 114836 116595: contig of 1760 bp in length
* 116596 116610: gap of unknown length
* 116611 118501: contig of 1891 bp in length
* 118502 118516: gap of unknown length
* 118517 229269: contig of 110753 bp in length.
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        /db_xref="taxon:9606"
        /clone="DJ1059M17"
BASE COUNT 60819 a 55407 c 54893 g 57758 t 392 others
ORIGIN

Query Match      20.7%; Score 30.4; DB 18; Length 229269;
Best Local Similarity 59.1%; Pred.No.6.3;
Matches 52; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 27 tgccttgaggccacagcagctctgtgagtcctctgtgggggtggaggtgggacaaagg 86
Db ~22104 TGCATTCCAGGACAGCAGCGTGTCTTAGTCACAGGATGAGATAGGATAGCACAAGGT 22045

Qy 87 aaaggggtgaatgtactgtgattaca 114
Db 22044 ACAGGTCACAAAGACCTTGCTGATAAAA 22017

RESULT 14
AC005075/c
LOCUS AC005075 198776 bp DNA HTG 12-JUN-1998
DEFINITION *** SEQUENCING IN PROGRESS *** Homo sapiens clone RG219E16; HTGS
phase 1, 3 unordered pieces.
ACCESSION AC005075
NID G3212916
KEYWORDS HTG; HTGS_PHASE1.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 198776)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-1998) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT *** WARNING: Phase 1 High Throughput Genome Sequence ***
***
* This sequence is unfinished. It consists of 3 contigs for
* which the order is not known; their order in this record is
* arbitrary. In some cases, the exact lengths of the gaps
* between the contigs are also unknown; these gaps are presented
* as runs of N as a convenience only. When sequencing is complete,
* the sequence data presented in this record will be replaced
* by a single finished sequence with the same accession number.
* 1 1784: contig of 1784 bp in length
* 1785 1801: gap of unknown length
* 1802 18710: contig of 16909 bp in length
* 18711 18727: gap of unknown length
* 18728 198776: contig of 180049 bp in length.
FEATURES
    Location/Qualifiers

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    /db_xref="taxon:9606"
    /clone="RG219E16"
BASE COUNT 60792 a 36795 c 37289 g 63866 t 34 others
ORIGIN

Query Match      20.7%; Score 30.4; DB 18; Length 198776;
Best Local Similarity 59.1%; Pred.No.6.3;
Matches 52; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 27 tgccttgaggccacagcagctctgtgagtcctctgtgggggtggaggtgggacaaagg 86
Db 183095 TGCATTCCAGGACAGCAGCGTGTCTTAGTCACAGGATGAGATAGGATAGCACAAGGT 183036

Qy 87 aaaggggtgaatgtactgtgattaca 114
Db 183035 ACAGGTCACAAAGACCTTGCTGATAAAA 183008

RESULT 15
AC003112
LOCUS AC003112 40668 bp DNA PRI 21-NOV-1997
DEFINITION Human DNA from chromosome 19 specific cosmid R30292, genomic
sequence, complete sequence.
ACCESSION AC003112
NID G2636669
KEYWORDS HTS.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 40668)
AUTHORS Lamerdin,J.E., McCreedy,P.M., Adamson,A.W., Burkhardt-Schultz,K.,
Gordon,L., Christensen,M., Kyle,A., Ramirez,M., Stillwagen,S.,
Garnes,J., Danganan,L., Bruce,R., Quan,G., Montgomery,M., Ow,D.,
Kobayashi,A., Olsen,A.O. and Carrano,A.V.
TITLE Sequence analysis of an ~1 Mb region containing the MEF2B gene in
19p12
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 40668)
AUTHORS Lamerdin,J.E.
TITLE Direct Submission
JOURNAL Submitted (21-NOV-1997) Human Genome Center, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
FEATURES
    source
        1. .40668
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        /cell_line="5HL2-B"
        /clone_lib="LL19NCO3 R chromosome 19 cosmid library"
        /note="LL19NCO3 cosmid library constructed at LLNL from
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        /note="predicted exon, program: grill2exons_human_1.3,
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        /note="HERV9 retroviral sequence"
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        misc_feature
        misc_feature
        LTR
        repeat_region
        repeat_region

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repeat_region 8951..9254
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repeat_region 9358..9535
/rpt_family="LTR12"
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misc_feature complement(9629..9672)
/note="predicted exon, program: grill2exons_human_1.3,
frame: 1, quality: excellent, score: 75.000"
repeat_region complement(9928..10123)
/rpt_family="Alu"
misc_feature 10409..10548
/note="DDS similarity to AA047548 zf15e02.rl Soares fetal
heart NBHH19W Homo sapiens cDNA clone 377018 5' (1..138);
96% identity.--Other overlapping matches:--(10435..10548)
DDS similarity to AA136115 zk90b04.rl Soares pregnant
uterus NBHPU Homo sapiens cDNA clone 490063 5' (1..110);
93% identity.--(10466..10548) DDS similarity to AA452628
zk33f04.rl Soares total fetus NB2HF8 9w Homo sapiens cDNA
clone 788287 5' (1..82); 95% identity.--(10486..10548) DDS
similarity to AA009412 ze82h02.rl Soares fetal heart
NBHH19W Homo sapiens cDNA clone 365523 5' (1..61); 97%
identity."
misc_feature 10643..10725
/note="predicted exon, program: grill2exons_human_1.3,
frame: 1, quality: excellent, score: 100.000--DDS
similarity to AA047548 zf15e02.rl Soares fetal heart
NBHH19W Homo sapiens cDNA clone 377018 5' (139..221); 100%
identity.--DDS similarity to AA136115 zk90b04.rl Soares
pregnant uterus NBHPU Homo sapiens cDNA clone 490063 5'
(111..192); 99% identity.--DDS similarity to AA452628
zk33f04.rl Soares total fetus NB2HF8 9w Homo sapiens cDNA
clone 788287 5' (83..165); 100% identity.--DDS similarity
to AA009412 ze82h02.rl Soares fetal heart NBHH19W Homo
sapiens cDNA clone 365523 5' (62..144); 100% identity."
misc_feature 11127..11331
/note="DDS similarity to AA136115 zk90b04.rl Soares
pregnant uterus NBHPU Homo sapiens cDNA clone 490063 5'
(193..394); 94% identity.--DDS similarity to AA009412
ze82h02.rl Soares fetal heart NBHH19W Homo sapiens cDNA
clone 365523 5' (145..346); 96% identity.--(11121..11331)
DDS similarity to AA009693 ze82h02.sl Soares fetal heart
NBHH19W Homo sapiens cDNA clone 365523 3' (429..307); 95%
identity.--(11127..11246) DDS similarity to AA047548
zf15e02.rl Soares fetal heart NBHH19W Homo sapiens cDNA
clone 377018 5' (222..341); 97% identity.--(11061..11331)
predicted exon, program: grill2exons_human_1.3, frame: 0,
quality: good, score: 73.000--(11061..11209) DDS
similarity to AA452628 zk33f04.rl Soares total fetus
NB2HF8 9w Homo sapiens cDNA clone 788287 5' (167..313);
98% identity."
repeat_region complement(11869..12161)
/rpt_family="Alu"
misc_feature 12502..12581
/note="DDS similarity to AA136115 zk90b04.rl Soares
pregnant uterus NBHPU Homo sapiens cDNA clone 490063 5'
(395..477); 92% identity.--DDS similarity to AA009412
ze82h02.rl Soares fetal heart NBHH19W Homo sapiens cDNA
clone 365523 5' (347..427); 94% identity.--DDS similarity
to AA009693 ze82h02.sl Soares fetal heart NBHH19W Homo
sapiens cDNA clone 365523 3' (306..228); 99%
identity.--DDS similarity to AA450010 zk33f04.sl Soares
total fetus NB2HF8 9w Homo sapiens cDNA clone 788287 3'
(309..229); 99% identity."
repeat_region complement(12966..13240)
/rpt_family="Alu"
repeat_region complement(13274..13531)
/rpt_family="Alu"
complement(13756..14029)
/note="predicted exon, program: grill2exons_human_1.3,
frame: 2, quality: good, score: 61.000--Other overlapping
matches:--(13756..13826) DDS similarity to AA009412
ze82h02.rl Soares fetal heart NBHH19W Homo sapiens cDNA
clone 365523 5' (428..496); 97% identity.--(13756..13984)
DDS similarity to AA009693 ze82h02.sl Soares fetal heart
NBHH19W Homo sapiens cDNA clone 365523 3' (227..1); 98%
identity.--(13756..13984) DDS similarity to AA450010
zk33f04.sl Soares total fetus NB2HF8 9w Homo sapiens cDNA
clone 788287 3' (228..1); 99% identity.--"
repeat_region complement(14100..14672)
/rpt_family="Alu"
misc_feature 14885..15317
/note="DDS similarity to AA046406 zvll07.sl Soares NBHMPU
S1 Homo sapiens cDNA clone 753348 3' (1..433); Score: 858
identity: 431/433 (99%).--(14884..15237) DDS similarity
to W37175 zb21a02.rl Soares fetal lung NBHL19W Homo
sapiens cDNA clone 302666 5' (1..355); 94%
identity.--(15227..14885) DDS similarity to AA121532
zk89c11.sl Soares pregnant uterus NBHPU Homo sapiens cDNA
clone 490004 3' (342..1); 99% identity.--(15227..14885)
DDS similarity to AA127694 zk89c11.rl Soares pregnant
uterus NBHPU Homo sapiens cDNA clone 490004 5' (126..467);
99% identity.--(15227..14897) DDS similarity to W46603
zc32h10.rl Soares senescent fibroblasts NBHSF Homo sapiens
cDNA clone 324067 5 (328..1); 98%
identity.--(15227..15088) DDS similarity to W46604
zc32h10.sl Soares senescent fibroblasts NBHSF Homo sapiens
cDNA clone 324067 3' (322..465); 96% identity."
misc_feature 15713..15760
/note="DDS similarity to AA121532 zk89c11.sl Soares
pregnant uterus NBHPU Homo sapiens cDNA clone 490004 3'
(399..343); 99% identity.--DDS similarity to AA127694
zk89c11.rl Soares pregnant uterus NBHPU Homo sapiens cDNA
clone 490004 5' (77..125); 90% identity.--(15735..15713)
DDS similarity to W46603 zc32h10.rl Soares senescent
fibroblasts NBHSF Homo sapiens cDNA clone 324067 5'
(351..329); 100% identity.--(15735..15713) DDS similarity
to W46604 zc32h10.sl Soares senescent fibroblasts NBHSF
Homo sapiens cDNA clone 324067 3' (299..321); 100%
identity."
misc_feature complement(15895..16082)
/note="predicted exon, program: grill2exons_human_1.3,
frame: 0, quality: excellent, score: 81.000--Other
overlapping matches:--(15936..15895) DDS similarity to
AA121532 zk89c11.sl Soares pregnant uterus NBHPU Homo
sapiens cDNA clone 490004 3' (431..390); 100%
identity.--(15970..15895) DDS similarity to AA127694
zk89c11.rl Soares pregnant uterus NBHPU Homo sapiens cDNA
clone 490004 5' (1..76); 100% identity."
repeat_region 17926..18190
/rpt_family="Alu"
misc_feature complement(18270..18438)
/note="predicted exon, program: grill2exons_human_1.3,
frame: 0, quality: excellent, score:
100.000--(18438..18284) DDS similarity to W66776
mel17b11.rl Soares mouse embryo NBME13.5 14.5 Mus musculus
cDNA clone 387741 5' similar to PIR:B38252 B38252
granulocyte colony-stimulating factor receptor precursor
(157..1); 82% identity.--(18438..18406) DDS similarity to
AA049280 mj45d02.rl Soares mouse embryo NBME13.5 14.5 Mus
musculus cDNA clone 479043 5' similar to SW:IL6B_MOUSE
Q00560 INTERLEUKIN-6 RECEPTOR BETA PRECURSOR (432..464);
88% identity."
misc_feature complement(18540..18697)
/note="predicted exon, program: grill2exons_human_1.3,
frame: 1, quality: excellent, score: 100.000--DDS
similarity to W66776 mel17b11.rl Soares mouse embryo
NBME13.5 14.5 Mus musculus cDNA clone 387741 5' similar to
PIR:B38252 B38252 granulocyte colony-stimulating factor
receptor precursor (316..158); 92% identity.--DDS
similarity to AA049280 mj45d02.rl Soares mouse embryo

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